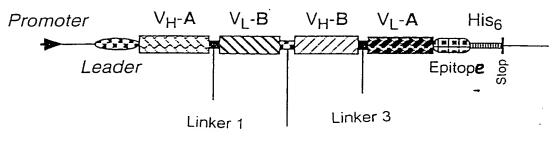
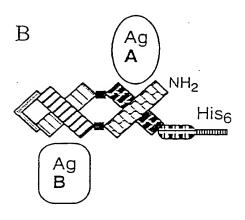
1/10

A



Linker 2



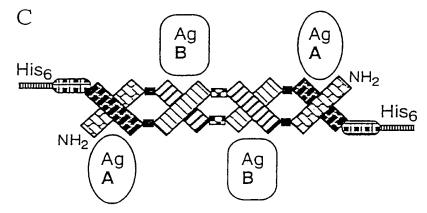


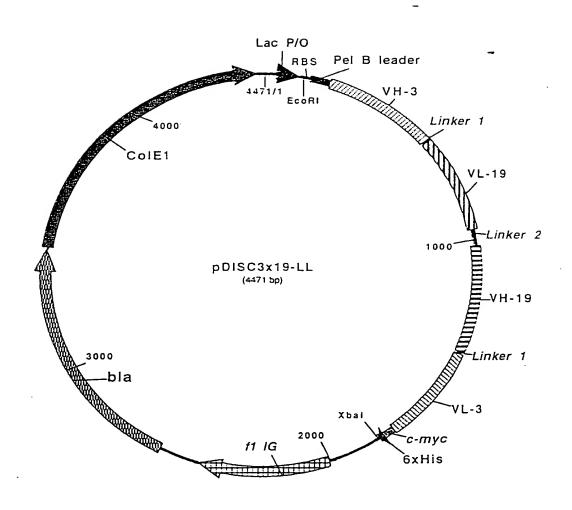
FIGURE 1

Linkers:

L1 = GG

 $L2 = (G_4S)_4$ 

L3 = GGPGS



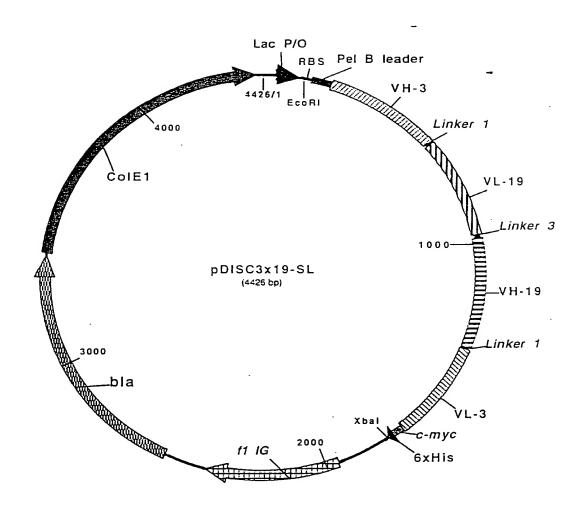


FIGURE 4

## 5/10

EcoRI RBS PelB leader Ncol
1 GAATTCATTAAA <u>GAGGAG</u> AAATTAACCA TGAAATACCTTATTGCCTACGGCAGCCGCTTGCTGCTGCTGCTGCAGCAGCTCAGCAGCCAATCG
I M K Y D E P T A A A G L E E A A Q P A M
• Frame-H1 VH anti-CD3
92 CGCAGGTGCAACTGCAGCAGTCTGGGGCTGAACTGGCAACGCCTGGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTTAC 22 A Q V Q L Q Q S G A E L A R P G A S V K M S C K A S G Y T F T
CDR-H1 Frame-H2 CDR-H2
183 TAGGTACACGATGCACTGGGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGATACATTAATCCTAGCCGTGGTTATAC
52 RYTMHWVKQRPGQGLEWIGYINPSRGYT Frame-H3
257 TAATTACAATCAGAAGTTCAAGGACAAGGCCACGTTGACTACAGACAAATCCTCCAGCACAGCCTACATGCAACTGAGCAGCCCTCAC
30 N Y N Q K F K D K A T L T T D K S S T A Y M Q L S S L T  CDR-H3  Frame-H4
354 ATCTGAGGACTCTGCAGTCTATTACTGTGGAAGA <u>TATTATGATGATCATTACAGCCTTGACTAC</u> TGGGGCCAAGGCACCACTCTCA
109) SEDSAVYYCARYYDD HYSLDYWG Q G TTL
CH1 Linker 1 Frame-L1 VL anti-CD19
440 CAGTOTOCTCA <u>GGCAAAACAACACCCC</u> AAGGTTGGGGGTGATATCTTGGTCACCCAAACTCCAGGTTCTTTGGGTGTGTGT
138 T V S S A K T T P K L G G D I L L T Q T P A S L A V S L G Q
CDR-L: Frame-L2 530 GGGCCACCATCTCCTGC <u>AAGGCCAGCCAAAGTGTTGATTATGATGGTGATAGTTATTTGAAC</u> TGGTACCAACACATTCCAGGAC
168 R A T I 5 C K A S Q S V D Y D G D S Y L N W Y Q Q I P G
CDR-L2 Frame-L3
614 AGCCACCCAAACTCCTCATCTATGATGCAATCCAATCTAGTTTCTGGGATCCCACCCA
196 Q P P K L L I Y D A S N L V S G I P P R F S G S G S G T D F COR-L3 Frame-L4
702 CACCOTCAACATCCATCCTGTGCACAAGGTGGATGCTGCAACCTATCACTGTCAGCAAAAGTACTGAGGATCCGTGGAACGTTCGGTGGA
225 TLNIH PYEK V DAATYH CQQSTED PWTFGG
Ckacca Notl Linker 2
790 GGCACCAAGCTGGAAATCAAA <u>CCGGGCTGATGCT</u> GCGGCCGGTGGTGGTGGTGGTTCTGGCGGCGGTGGTAGCGGTGGTGGCGGC
255 GTKLEIKRADAAAAGGGGSGGGGG Pvull Frame-H1 VH anti-CD19
874 TCCGGTGGTGGTGGTAGCCAGCTGCAGCTGCAGCAGTCTGGGGCTGAGCCTGGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGG
283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K
283 S G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K CDR-H1 Frame-H2 CDR-H2
283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K  CDR-H1 Frame-H2 CDR-H2  962 CTTCTGGCTATGCATTCAGT <u>AGCTACTGGATGAAC</u> TGGGTGAAGCAGCGTGAACAGGGTCTTGAGTGGATTGGACAGACTTGGGC
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K  CDR-H1 Frame-H2 CDR-H2  962 CTTCTGGCTATGCATTCAGT <u>AGGTACTGGATGAAC</u> TGGGTCAAGCAGGCTCTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGC  312) A S G Y A F S S Y W M N W V K Q R P G Q G L E W I G Q I W
283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K  CDR-H1 Frame-H2 CDR-H2  962 CTTCTCGCTATCCATTCAGTAGCTACTGGATGAACTGGGTCAAGCCCTCGACAGGGTCTTCAGTGGATTGGACAGATTTGGC  312 A S G Y A F S S Y W M N W V K Q R P G Q G L E W I G Q I W  Pstl Frame-H3
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K  CDR-H1  Frame-H2  962 CTTCTCCCTATCCATTCAGTAGCTACTGGATGAACTGGGTCAAGCCACAGCCTCCAACAGCGTCTTCAGTGGATTTGGC  312 A S G Y A F S S Y W M N W V K Q R P G Q G L E W I G Q I W  Pstl Frame-H3  1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTCGACTGCAGCACGACTCACCCCTACA  341 P G D G D T N Y N G K F K G K A T L T A D E S S S T A Y
283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K  CDR-H1 Frame-H2 CDR-H2  962 CTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAACCACAGGCCTGGACAGGGTCTTGAGTGGATTGGACAGAGATTTGGC  312 A S G Y A F S S Y W M N W V K Q R P G Q G L E W I G Q I W  PStl Frame-H3  1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGACGACCAATCCTCCAGCACACCCTACA  341 P G D G D T N Y N G K F K G K A T L T A D E S S S T A Y  CDR-H3
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K  CDR-H1  Frame-H2  962 CTTCTCCTATCCATTCAGTAGCTACTGGATGAACTGGGTCAAGCACAGGGTCTTGAGTGGATTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTTGGACAGAGTTGGACAGACTTGACTGCAGACGAATCCTCCAGCACAGCCTACA  1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGACGAATCCTCCAGCACAGCCTACA  141) P G D G D T N Y N G K F K G K A T L T A D E S S T A Y  CDR-H3  1133 TGCAACTCAGCAGCCTAGCATCTGCGGACTCTGCGGTCTATTTCTGTGCAAGACGGGGAGACTACGACGGTAGGCCGTTATTACTAT
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K  CDR-H1  Frame-H2  962 CTTCTCCTATCCATTCAGTAGCTACTGGATGAACTGGGTGAACCACACGCTTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGC 312) A S G Y A F S S Y W M N W V K Q R P G Q G L E W I G Q I W  PStl Frame-H3  1049 CTGGAGATGGTGATACTAACAATGGAAAGTTCAAGGGTAAAGCCACTTGACTGCAGACGAATCCTCCAGCACAGCCTACA 341) P G D G D T N Y N G K F K G K A T L T A D E S S S T A Y  CDR-H3  1113 TGCAACTCAGCACCCTAGCATCTGAGGACTCTTGCGGTCTATTTCTGTGCAAGACGGGGAGACTACGACGGTAGGCCGTTATTACTAT 369) M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K  CDR-H1  Frame-H2  CDR-H2  962 CTTCTCCCTATCCATTCACTAGCTACTGGATGGATGGATG
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K  CDR-H1  Frame-H2  962 CTTCTCCTATCCATTCAGTAGCTACTGGATGAACTGGGTGAACCACACGCTTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGC 312) A S G Y A F S S Y W M N W V K Q R P G Q G L E W I G Q I W  PStl Frame-H3  1049 CTGGAGATGGTGATACTAACAATGGAAAGTTCAAGGGTAAAGCCACTTGACTGCAGACGAATCCTCCAGCACAGCCTACA 341) P G D G D T N Y N G K F K G K A T L T A D E S S S T A Y  CDR-H3  1113 TGCAACTCAGCACCCTAGCATCTGAGGACTCTTGCGGTCTATTTCTGTGCAAGACGGGGAGACTACGACGGTAGGCCGTTATTACTAT 369) M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K  CDR-H1  Frame-H2  962 CTTCTGGCTATGCATTCAGTAGGTAGGATGGATGGATGGA
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K  CDR-H1  Frame-H2  962 CTTCTGGCTATGCATTCAGTAGGTAGTGGATGGATGGATG
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V K I S C K  CDR-H1  Frame-H2  962 CTTCTGCTATGCATTCAGTAGGTACTGGATGAACTGGGTGAACAGCACAGCCTTGACAGACA
283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X  CDR-H1  Frame-H2  CDR-H2  962 CTTCTGCCTATGCATTCAGTAGCTACTGGATGAACTGGGTCAAGCACAGCCTTGACAGGGTCTTGAGTGGATTGGACAGAGTTTGGC  312 A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W  PSII Frame-H3  1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCAGACGAACCTCCAGCCTACA  341 P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y  CDR-H3  1133 TGCAACTCAGCACCTTGAGGACTCTGGGGTCTATTTCTGTGCAAGAGGGGAGACTACGACGGTAGGCGGTTATTACTAT  369 M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y  Frame-H4  CH1  Linker 1 Frame-L1  1219 GCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCACCTCAAGCAAACAACACCAAGCTTGGCGGTGATATCGTCCTCACCTAAACAACAACCACCAAGCTTGGCGGTGATATCGTCCTCACCTAAACAACAACCAAC
283 S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X  CDR-H1  Frame-H2  CDR-H2  962 CTTCTGGCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAACCAGAGCCTTGAACGGGTCTTGAGTGGATTGGACAGAGTTTTGGC  312 A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W  PStI Frame-H3  1049 CTGGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACCCAATCCTCAGCCAACCCTACA  341 P G D G D T N Y N G K F K G K A T L T A D E S S S T A Y  CDR-H3  1133 TGCAACTCAGCAGCCTAGCATCTGAGGACTCTGGCGGTAGGCCGTTATTACTAT  369 M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y Y  Frame-H4  CH1  Linker 1 Frame-L1  1219 GCTATGGACTACTGGGGTCAAGGACCTCAGTCACCGTCTCACCCGAAACAACACCCAAGCTTGGCGGTGATATCGTGCTCACTC  398 A M D Y W G Q G T S V T V S S A K T T P K L G G D I V L T  VL anti-CD3  CDR-L1  1307 AGTCTCAGCAATCATCTGCATCTCAGGGGAAGGTCACCATGACCTGAGGTGCAAGTTAAGTTACATGAACTGG  427 Q S P A I M S A S P G E K V T M T C S A S S S V S Y M N W  Frame-L2  CDR-L2  Frame-L3  1393 TACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATCCAACACTGGCTTCTCACGGGCGA
CDR-H1  Frame-H2  CDR-H2  962 CTTCTGCCTATGCATTCAGTAGCTACTGGATGAACTGGGTGAACGGGGTGAAAGGGGTCTTGAGTGGATGACAGAGGTTTGGC  312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W  PSII Frame-H3  1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTCTGACTGCACACGAATCCTCAACCAGCCTACA  341) P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y  CDR-H3  1133 TGCAACTCAGCAGCCTAGCATCTGAGGACTACTGCGGTCATTTCTGTGCAACAGGGGAGAGCTACGACGGGTAGGCCGTTATTACTAT  369) M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y  Frame-H4  CH1  Linker 1 Frame-L1  1219 GCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCGCAAAACAACCAAACCTTGGGGGTGATATCGTGCTACTC  398) A M D Y W G Q G T S V T V S S A X T T P X L G G D I V L T  VL anti-CD3  CDR-L1  1307 AGTCTCAGCAATCATGTCTGCATCTCAGGGCAAGGTCACCAACCTTGGGGGTGATATCATGAACTGG  427) Q S P A I M S A S P G E X V T M T C S A S S S V S Y M N W  Frame-L2  CDR-L2  Frame-L3  1393 TACCAGCAGAAGTCAGGCACCTCCCCCAAAAAGATGGATTTCATGGAACTTCAGGGGCAA
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X  COR-H1 Frame-H2 CDR-H2  962 CTMCTGCTATCATTGCTAGCTAGCTAGCTGGATGAACTGGGATGAACTGGCCTGGACAGGGTCTTGAGTGGATTGGCAGAGATTTGGC 312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W  PSII Frame-H3  1049 CTGGGAGATGGTGATAACTAACTACAATGGAAAGTTCAAGGGTAAAGCCACTGCACTGACTG
CDR-H1  Frame-H2  CDR-H2  962 CTMCTGCTATGCATTCAGTAGCTAGGGATGAACTGGGGGGGAACTCTGACCGGGATGGGATGGACTGGACAGGCTTGAGGATGGAT
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X  CDR-H1  Frame-H2  CDR-H2  962 CTTCTCCCTATCCATTCACTGCTACTGGATGACTCCACTCCACCCCCACACCCTTCACCGCACACCTTCACTGCACTGGCC  312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W  PSII Frame-H3  1049 CTGGAGATGGTGATACTACACTACACACCTCACACACCTCCACCCCACACCCTCCACACCTTCACCCCACACCAC
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X  CORHI  Frame-H2  CDR-H2  962 CTTCTGCTATGCATTCAGTAGCTAGGAACTGGAACTGGGATGGACTGGGCCTGGACAGGGCTTGAGGGGTTGGACAGGCCTGGACTTGGGCGATTTGGC 312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W  PStI Frame-H3  1049 CTGGAGATGGTGATACTACAACTGGAAAGTTCAAGGGTAAAGCCACTACTCACAGCAAATCCTCAGCACAACTCTCACACCAACTCACCACACCACCCTACA 341) P G D G D T N Y N G X F X G X A T L T A D E S S S T A Y  CDR-H3  1133 TGCAACTCAGCAGCCTAGCATCTGAGGACTTCCGGGTCTATTTCTGTCAAGACGGGAGACTACGACGGTAGGCCGTTATTACTAT 369) M Q L S S L A S E D S A V Y F C A R R E T T T V G R Y Y Y  Frame-H4  CH1  Linker 1 Frame-L1  1219 GCTATGGACTACTGGGGTCAAGGACCTCAGTCACCCGACACACCCCCAAGCTTGGCGGTGATTACTGACTCACTC
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X  CDR-H1  Frame-H2  CDR-H2  962 CTTCTCCCTATCCATTCACTGCTACTGGATGACTCCACTCCACCCCCACACCCTTCACCGCACACCTTCACTGCACTGGCC  312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W  PSII Frame-H3  1049 CTGGAGATGGTGATACTACACTACACACCTCACACACCTCCACCCCACACCCTCCACACCTTCACCCCACACCAC
283) S G G G G S Q V Q L Q Q S G A E L V R P G S S V X I S C X  CORHI  Frame-H2  CDR-H2  GCR-H2  962 CTTCTCCCTATCCATTCACTGCATCTCGGTAGAACTCGGTCAACCACGCCTCGACACGGGTCTTCAGTGGATTCACCAGATTTGGC  312) A S G Y A F S S Y W M N W V X Q R P G Q G L E W I G Q I W  PSII Frame-H3  1049 CTGGAGATGGTGATACTAACTACAATGGAAAGTTCAAGGGGTAAAGCCACTCTCACACACA
COR-HI

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EcoRI RBS PelB leader Ncol
EGY/COSCOCRACTICALOSTOSTOSTOSTOSTOSTOSCOS/COSCACATOCATACOSTACACATACA SA ACALACAGA ACALACAGA ACALTICACTICA E
PMXYLLPTAAAGLELLAAQ.PAM
Frame-H1 VH anti-CD3
92 CGCAGGTGCAACTGCAGCAGTCTGGGGCTGAACTGGCAAGACCTGGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACCTTTTAC
22) A Q V Q L Q Q S G A E L A R P G A S V K M S C K A S G Y T F T  CDR-H1 Frame-H2 CDR-H2
183 TAGGTACACGATGCACTGCGTAAAACAGAGGCCTGGACAGGGTCTGGAATGGATTGGATACATTAATCCTAGCCGTGGTTATAC
52) RYTMHWVKQRPGQGLEWIGYINPSRGYT
Frame-H3 267 <u>TAATTACAATCAGAAGTTCAAGGAC</u> AAGGCCACATTGACTACAGACAAATCCTCCAGCACAGCCTACATGCAACTGAGCAGCCTGAC
20) IN Y N Q K F K D K A T L T T D K S S S T A Y M Q L S S L T
CDR-H3 Frame-H4
CDH-HS 354 ATCTGAGGACTCTGCAGTCTATTACTGTGCAAGA <u>TATTATGATGATCATTACAGCTTTGACTACTACTACCCACCC</u>
109 SEDSAVYYCARYYDDHYSLDYWGQGTTL
CH1 Linker 1 Frame-Li VL anti-CD19
440 CAGTCTCCTCAGCCAAAACAACACCCAAGCTTGGGGGGTGATATCTTGCTCACCCAAACTCCAGCTTCTTTGGCTGTGTCTCTAGGGCAGA
133) T V S S A K T T P K L G G D I L L T Q T P A S L A V S L 3 Q
CDR-L1 Frame-L2
530 GGGCCACCATCTCCTGCAAGGCCAAAGTGTTGATTATGATGATGATGATATTTGAACTGCTACCAACAGATTCCAGGAC 168 R A T I S C K A S Q S V D Y D G D S Y E N W Y O C I F G
CDR-L2 Frame-L3 614 AGCCACCCAAACTCCTCATCTAT <u>GATGCATCCAATCTAGTTTCTGGCACCCAGGTTTAGTGGCAGTGGGTCTGGGACAG</u> ACTT
196 Q P P K L L I Y D A S N L V S G I P P R F S G S G S G T D F
CDR-L3 Frame-L4
702 CACCCTCAACATCCATCCTGTGGAGAACGTGGATGCTGCAACCTATCACTGT <u>CAGGAAAAGTACTGAGGAT</u> CCGTCGACGTTCGGTGGA
225° TLNIH PVEKVDAATYHCQQSTEDPWTFGG
Ckappa Notl Linker 3 Pvutl Frame-H1
790 GGCACCAAGCTGGAAATCAAA <u>CGCCCCTAATGCT</u> GCGGGCCCTGGTGGGCCCAGGGTGCAGGTGCAGCTGCAGCAGTCTGGGGCTGAGCT
790 GGCACCAAGCTGGAAATCAAA <u>CGCCCCTGATSCTT</u> GCSGCCCCTGGTGGCCCAAGGTGCAGCTGCAGCAGCAGCAGCAGCCTGAGCT 255 G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L
255 G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19 CDR-H1 Frame-H2
255 G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L  VH anti-CD19  CDR-H1 Frame-H2  879 GGTGAGGCCTGGGTGAACATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGC
255 G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L  VH anti-CD19  CDR-H1  Frame-H2  879 GGTGAGGCCTGGGTCCTCAGTGAACATTTCCTGCCAAGGCTTCTGGCTTATGCATTCAGTGAGCTAGTGGATGAACTGGGTCAAGCAAG
255 G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  879 GGTGAGGCCTGGGTGAGGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAG
255 G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  879 GGTGAGGCCTGGGTCATGAACATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGTGAAGTTGAACTGGGTAAGCAGGCC  284 V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTTTGAGTGGATTTGGACAGATTTGGCCTGGAGATGAATTGAACTAACT
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAAGTGAAGTGGAAGCTGGGTGAAGCAGGCC 284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTTTGGACTGGATTTGGCCTGGAGATTTGGCTGAAGTGAAGTTCAAGGGTAAGCC 314) P G Q G L E W I G Q I W P G D G D T N Y N G K F K G K A
255) G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  879 GGTGAGGCCTGGGTCATGAACATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGTGGATGAACTGGGTAAGCAGGCC  284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTTTGGACTGGATTTGGACAGATTTGGCCTGGGAGATGGTAACTAAC
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  379 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGGTGATGAAGCTGGAGGCC  284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTTTGGACAGATTTTGGCTGGAGATTTGGCTGAAGATTGAATTGAAAGTTCAAGGGTAAAGCC  314) P G Q G L E W I G Q I W P G D G D T N Y N G K F K G K A  Frame-H3  1051 ACTCTGACTGCAGAGAGATTCCTCAGCACAGCCTACATCCAACTCCAGCACTCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAC
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGGTGATGAAGCTGGAAGCAGAGCC  284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGAGATGGTGATACTAAATTGAAATGGAAAGTTCAAGGGTAAGCC  314) P G Q G L E W I G Q I W P G D G D T N Y N G K F K G K A  Frame-H3  1051 ACTCTGACTGCAGAGCGAATCCTCAGCACCCTACATCCAACTCAGCACCTTAGCATCTGAGGACTCTGCGGTCTATTTCTGTGCAAGAC  342) T L T A D E S S S T A Y M Q L S S L A S E D S A V Y F C A R
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGTGGATGAACTGGGTGAAGCAGAGCC 284) V R P G S S V X I S C X A S G Y A F S S Y W M N W V X Q R  CDR-H2  968 CTGGACAGGGTCTTGAGTGGATTGGACAGATTTTGGCCTGGAGATGGTGATGCAATGGAAAGTTCAAGGGTAAAGCC 314) P G Q G L E W I G Q I W P G D G D T N Y N G X F K G X A  Frame-H3  1051 ACTCTGACTGCAGACGAATCCTCCAGCACTACATGCAACTCAGCAGCCTTAGGACTCTGAGGACTCTGGGGTCTATTTCTGTGCAAGAC 342) T L T A D E S S T A Y M Q L S S L A S E D S A V Y F C A R  CDR-H3  CCH1
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGGTGATGAACTGGGTGAAGCAGGCC  284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTCTTGAGTGGATTTGGACAGATTTGGCCTGGAGATGGTGATGCAATGGAAAGTTCAAGGGTAAAGCC  314) P G Q G L E W I G Q I W P G D G D T N Y N G K F K G K A  Frame-H3  1051 ACTCTGACTGCAGACGAATCCTCCACAGCCTACATCCAACTCAGCAGCCTAGGACTCTGAGGACTCTGGGGTCTATTTCTGTGCAAGAC  342) T L T A D E S S S T A Y M Q L S S L A S E D S A V Y F C A R  CDR-H3  Frame-H4  CH1  1142 GGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTTACGGACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCAACCTCAGCCAAACAACCTCAGCAACCTCAGCAACCTCCAGCCCAACAACCTCAGCAACCTCAGCAACCTCAGCAACCTCCAGCCCTAACAACCTCAGCCAACAACCTCAGCAACCTCAGCAACCTCCAGCCCTCAACAACCAAC
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGCTAGTGGATGAACTGGGTGAAGCAGAGCC 284) V R P G S S V X I S C X A S G Y A F S S Y W M N W V X Q R  CDR-H2  968 CTGGACAGGGTCTTGAGTGGATTGGACAGATTTGGCCTGGGAGATGGTGATGCAAGTGAAAGTTCAAGGGTAAAGCC 314) P G Q G L E W I G Q I W P G D G D T N Y N G X F X G X A  Frame-H3  1051 ACTCTGACTGCAGACGAATCCTCACCACAGCCTACATCCAACTCAGCACCCTAGCATCTGAGGACTCTGGGGTCTATTTCTGTGCAAGAC 342) T L T A D E S S S T A Y M Q L S S L A S E D S A V Y F C A R  CDR-H3  Frame-H4  CH1  1142 GGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTTCCGGGTCTCACCGCCTACCCTACCACCCCACCCTCAGCCACCCCTCAGCCACCCCCAGCCACCCTCAGCCACCCCTCACCCCTCCACCCCTCCACCCCTCACCCCTCCACCCCTCCACCCCTCCACCCCTCACCCCTCCACCCCTCCACCCCTCCACCCCTCACCCCTCCACCCCTCACCCCTCCACCCCTCACCCCTCACCCCCTCACCCCTCCCTCCACCCCCC
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAG
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  379 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAG
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  879 GGTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTAGGTAG
VH anti-CD19  CDR-H1  Frame-H2  879  GGTGAGGCCTGGGTCTAGTGAAGATTTCCTGCAAGGCTTCTGGCTATGCATTCAGTGAGTG
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  379 GSTCAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGCCTATGCATTCAGTAGCTACTGGAAGATGAACTGGGAAGCCAGAGGC  284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTCTTGAGTGGATTGGACAGATTTTGGCTGGGATGATACTAACAATGGAAAGTTCAAGGGTAAAGCC  314) P G Q G L E W I G Q I W P G D G D T N Y N G K F K G K A  Frame-H3  1051 ACTCTGACTGCAGACGAATCCTCCAGCCTACATCCAACTCAGCACCTTAGCATCTGAGGACTCTTGCGGTCTATTTCTGTGCAAGAC  342) T L T A D E S S S T A Y M Q L S S L A S E D S A V Y F C A R  CDR-H3  Frame-H4  CH1  1142 GGGAGACTACGACGGTAGGCCGTTATTACTATGCTATGGACTTACTGGGTCACTCTCAGCCAACA  372) R E T T T V G R Y Y Y A M D Y W G Q G T S V T V S S A K  Linker 1 Frame-L1 VL anti-CD3  1226 CAACACCCAAGCTTGGGGTGATATCGTGCACCTCACTCAGCCAATCATCGCAACCTCCAGGGAAGGTCACCATGACCTGCA  400) T T P K L G G D I V L T Q S P A I M S A S P G E K V T M T C  CDR-L1  Frame-L2  CDR-L2
VH anti-CD19  CDR-H1  Frame-H2  879 GGTGAGCCTGGGTCTCAGTGAAGATTTCTGCAAGGCTTCTGGGTATGCATTCAGTAGCTACTGGGTGAAGCAGAGCGGGC  CDR-H2  968 CTGGACAGCCTCTGAGGATTTGACAGATTTCGGCTGGGGGGGG
255) G T K L E I X R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  379 GGTGAGGCCTGGGTCCTCAGGAACATTTCCTGCAACGCTTCTGCTATGCATTCAGTAGGATGAACTGGGTGAACATGAGCAGGCC  284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V K Q R  CDR-H2  968 CTGGACAGGGTCTTGAGTGGATTTGGACAGATTTGGCCTGGAGATGGTGATACTAACTA
255   G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19
255) G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L VH anti-CD19  CDR-H1  Frame-H2  379  GOTGAGGCCTGGGTCCTCAGGAAGATTCCTGCAAGCCTTCTGGCTATGCATTCAGTGGATGAACTGGATGAACTAGGAGGCC  284) V R P G S S V K I S C K A S G Y A F S S Y W M N W V X Q R  CDR-H2  968  CTGGACAGGGTCTTGAGTGGATTTGGACGAGATTTGGCCTGGAGATGATGAACTAACT
VH anti-CD19  VH anti-CD19  CDR-H1  Frame-H2  379 GGTGAGGCCTGGGGTCGTGAAGATTTCCTGCAAGCCTTCTGGCTATGCATTCAGTGAAGATGAACTGGGTAAGCAAGGGC 284) V R P G S S V X I S C K A S G Y A F S S Y W M N W V X Q R  CDR-H2  968 CTGGACAGGTCTTGAGTGAATTTGACAGATTTGGCCTGGAGATGAAGTGAATTCAAGTGGAAAAGTGAAATGGAAAGTGAAAGATGAAGTAACCC 314) P G Q G L E W I G Q Q I W P G D G D T N Y N G X F K G K A  Frame-H3  1051 ACTCTGACTGCAGACGAATCCTCCAGCACACCCTACATCCAACTCAGCACCTTGAGAACTCTGAGACTCTGGGGTCTATTTCTGTGCAAGAC 342) T L T A D E S S S T A Y M Q L S S L A S E D S A V Y F C A R  CDR-H3  1422 GGGAGACTACGACGGTTAGGACGGTTATTTACTATGGTATTGGACTACTCTGAGCACTCTGGGGCACACCTCAGCTCTCCTCAGCCTACACTCCAGCAACCTCAGCACCTCAGCACCTCAGCACCTCAGCACCTCAGCACCTCAGCACCTCAGCACCTCAGCACCTCAGCACCTCAGCACCTCAGCACCTCCAGCCACCACCACCACCACCACCACCCCAAGACCTCAGCACCTCAGCACCTCCCCCCAACACCTCAGCACCTCCCCCCCAACAACGTCACCCTCCCCCCCAACACCTCAGCACCCCCCCC
255) G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L  VH anti-CD19  CDR-H1  Frame-H2  379 GTGAGGCCTGGTTCCTCAGGAAGATTTCCTGCAAGGCTTCTGCCTATCATTCAGTAGGTAACTGGAAGATCGGTAAGAGGGC 284) V R P G S S V K I S C K A S G Y A F S S Y W M N N V X Q R  CDR-H2  968 CTGGACAGGTTCTGAGTGGATTTGGACAGTTTGGCTAGGCTTGAAGTTGAAATGGAAAGTTCAAGGGTAAAGCC 314) P G Q G L E W I G Q I W P G D G D T N Y N G K F K G K A  Frame-H3  1051 ACTCTGACTGCAGACAATCCTCCAGCCTACATGCAACTCAGCACCTTAGCACTTGAGGACTCTGCGGTCTATTTCTGGCAGGC 342) T L T A D E S S S T A Y M Q L S S L A S E D S A V Y F C A R  CDR-H3  1142 GGGAGACTACGACGAGGTGAGGCCGTTACTATCTATGGACTTCTGGGACCTTAGGACCTCAGCTAAGAG 372) R E T T T V G R Y Y Y A M D Y W G Q G T S V T V S S A K  Linker 1 Frame-L1 VL anti-CD3  1226 CAACACCCAAGCTTGGCGGTGATATCGTGCTCACTCAGCCAACCTCGCACCTCCAGCAAGAGGTCACCATGACCTGCA 400) T T P K L G G D I V L T Q S P A I M S A S P G E K V T M T C  CDR-L1  Frame-L2  1316 GTGCCAGGTCAAGTTGAAGTTACATGAACTCAGGCAAGGCACCCCCAAAAGATGGAACGTCACCATCACCTGCAA 430) S A S S S V S Y M N W Y Q Q K S G T S P K R W I Y D T S K  Frame-L3  1401 ACTGGCTTCTGGAGTGAAGTTACATGAACTCAGGGCAAGGCCCCAAAAGATGGACCTCAAGCATCCAACCTCCAACCATCCAACCTCCAAGCATCCAAGCATCCAACCTCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACCATCCAACC
255) G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L  VH anti-CD19  CDR-H1  Frame-H2  379 GGTGAGGCTGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGCTATGCATTCAGTGGTGAAGCTGATGGATG
255) G T K L E I K R A D A A A A G G P G S Q V Q L Q Q S G A E L  VH anti-CD19  CDR-H1  Frame-H2  379 GTGAGGCCTGGGTCCTCAGTGAAGATTTCCTGCAAGGCTTCTGCTATCATTCAGTAGCTAACTGGATAGCTGAAGAGCC 284) V R P G S S V K I S C K A S G Y A F S S Y W M N N W V X Q R  CDR-H2  968 CTGGACAGGCTTGGGTGGATTGGACAGATTTGGCTGGGAAGATGGAAAGTTGAAAGGGTAAAGCC 314) P G Q G L E W I G Q I W P G D G D T N Y N G K F K G K A  Frame-H3  1051 ACTCTGACTGGAGCAGAATCCTCCACCAGCCTACATGCAACTCAGCACCTTGCAACTTGAGGACTCTCCGGTCTATTTCTGGCAAGC 342) T L T A D E S S S T A Y M Q L S S L A S E D S A V Y F C A R  CDR-H3  1142 GGGAGACTACGAGCGGTAGGCCGTTACTTAGGACTTAGGACTCTCGGGACCTCAGCTCCTCCTCCTCAGCTAGAC 372) R E T T T V G R Y Y Y A M D Y W G Q G T S V T V S S A K  Linker 1 Frame-L1 VL anti-CD3  1226 CAACACCCAAGCTTGGCGGTGATATGGTCTCACTCAGCTACATCAGCACTCTCCAGCGGGAAGGTCACCATGACCTGCA 400) T T P K L G G D I V L T Q S P A I M S A S P G E K V T M T C  CDR-L1  Frame-L2  1316 GTGCCAGCTCAAGCTGGAGTTAACTTACATGAACTCCAGCAACTCAGCCCCCCCAAAAGATGGAACGTCACCATCCAAC 400) S A S S S V S Y M N W Y C Q K S G T S P K R W I Y D T S K  Frame-L3  1401 ACTGGCTTCTCGAGTCCAGCTCACTCAGGGCAACATCATGTCTCCCCCCAAAAGATGGATTTATGACACATCCAA 458) L A S G V P A H F R G S G S G T S Y S L T I S G M E A E D A  CDR-L3  Frame-L4  C COR-L3  Frame-L4  C CARCACCTAGCTTCTCGAGTCCCTCCACCTCACCTCACCT

941 ATGAGATTTCCTTCAATTTTTACTGCTGTTTTATTCGCAGCATCCTCCGCATTAGCTGCTCCAGTCAACACTAC 1 M R F P S I F T A V L F A A S S A L A A P V N T T alpha-factor signal 1015 AACAGAAGATGAAACGGCACAAATTCCGGCTGAAGCTGTCATCGGTTACTCAGATTTAGAAGGGGATTTCGATG 25) TEDETAQIPAEAVIGYSDLEGDF.D 1089 TTGCTGTTTTGCCATTTTCCAACAGCACAATAACGGGTTATTGTTTATAAATACTACTATTGCCAGCATTGCT 50 V A V L P F S N S T N N G L L F I N T T I A S I A m EcoRI Xhol 1163 CCTALAGAAGAAGGGGTATCTCTCGAGAAAAGAGAGGCTGAAGCT<u>GAATTC</u>CAGGTGCAACTGCAGCAGTC 75 A K E E G V S L E K R E A E A E F Q V Q L Q Q S VH anti-CD3 1 1234 TGGGGCTGAACTGGCAAGACCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCT 98 G A E L A R P G A S V K M S C K A S ij Ш i=

FIGURE 7

941 ATGAGATTTCCTTCAATTTTTACTGCTGTTTTATTCGCAGCATCCTCCGCATTAGCTGCTCCAGTCAACACTAC 1 M R F P S I F T A V L F A A S S A L A A P V N T T alpha-factor signal 1015 AACAGAAGATGAAACGGCACAAATTCCGGCTGAAGCTGTCATCGGTTACTCAGATTTAGAAGGGGATTTCGATG 25 TEDETAQIPAEAVIGYSDLEGDFD #1089 TTGCTGTTTTGCCATTTTCCAACAGCACAAATAACGGGTTATTGTTTATAAATACTACTATTGCCAGCATTGCT 50 V A V L P F S N S T N N G L L F I N T T I A S I A ٠Ų **EcoRI** Xhol 1163 GCTAAAGAAGAAGGGGTATCTCTCGAGAAAAGAGAGGGCTGAAGCT<u>GAATTC</u>ATGGCGCAGGTGCAACTGCAG 75 A K E E G V S L E K R E A E F M A Q V Q L Q VH anti-CD3 1235 CAGTCTGGGGCTGAACTGGCAAGACCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCT 99 Q S G A E L A R P G A S V K M Ü IJ O 4

FIGURE 8

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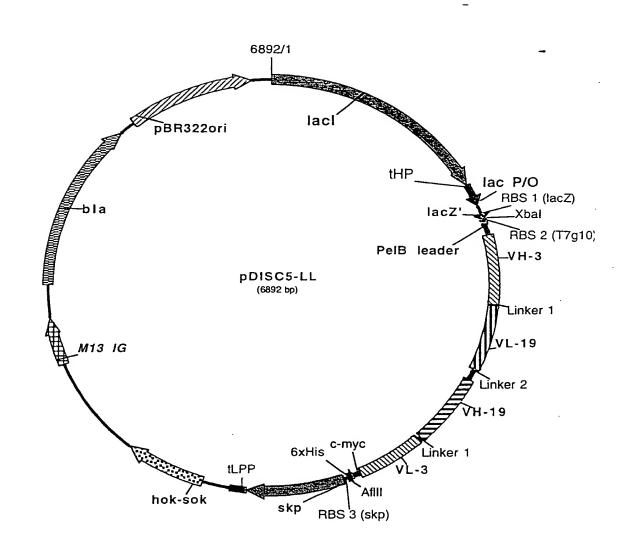


FIGURE 9

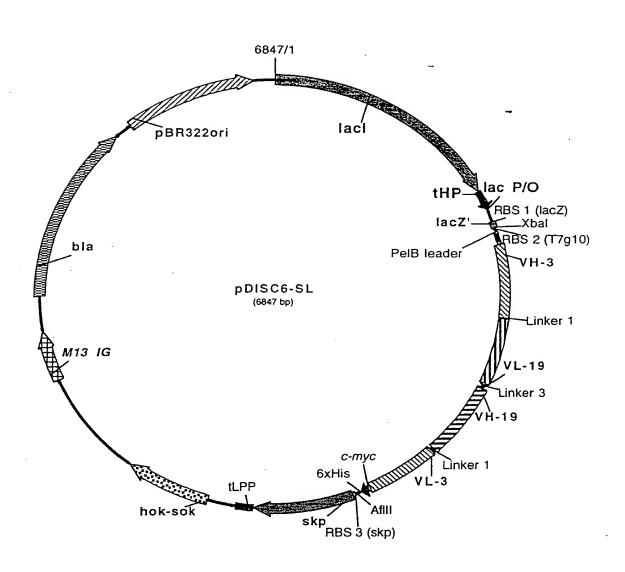


FIGURE 10